SEQUENCE LISTING

<110> KRÖHN, Kai
HEINO, Maarit
PETERSON, Part
SCOTT, Hamish
ANTONARAKIS, Stylianos
LALIOTI, Maria D.
SHIMIZU, Nobuyoshi D.
KUDOH, Jun D.

<120> NOVEL GENE DEFECTIVE IN APECED AND ITS USE

<130> u 012653-9

<140> 09/508,658
<141> 2000-11-03

<160> 41

<170> PatentIn version 3.2

<210> 1
<211> 2036
<212> DNA
<213> HOMO SAPIENS

<220>
<221> CDS
<222> (137)..(1771)
<223> /product="AIR-1"

<220>
<221> mat_peptide
<222> (1)..(545)
<223> /product="AIR-1"

<400> 1
agaccgggga gacgggcggg cgcacagccg gcgcggaggc cccacagccc cgccgggacc 60

cgaggccaag cgaggggctg ccagtgtccc gggacccacc gcgtccgccc cagccccggg 120

tccccgcgcc cacccc atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg 172
Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg
1 5 10

ctg cac cgc acg gag atc gcg gtg gcc gtg gac agc gcc ttc cca ctg 220
Leu His Arg Thr Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu
15 20 25

ctg cac gcg ctg gct gac cac gac gtg gtc ccc gag gac aag ttt cag 268

```
Leu His Ala Leu Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln
    30                  35                  40

gag acg ctt cat ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac      316
Glu Thr Leu His Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His
45                  50                  55                  60

gcc ctc ctg tcc tgg ctg ctg acc cag gac tcc aca gcc atc ctg gac      364
Ala Leu Leu Ser Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp
                65                  70                  75

ttc tgg agg gtg ctg ttc aag gac tac aac ctg gag cgc tat ggc cgg      412
Phe Trp Arg Val Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg
            80                  85                  90

ctg cag ccc atc ctg gac agc ttc ccc aaa gat gtg gac ctc agc cag      460
Leu Gln Pro Ile Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln
        95                  100                 105

ccc cgg aag ggg agg aag ccc ccg gcc gtc ccc aag gct ttg gta ccg      508
Pro Arg Lys Gly Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro
    110                 115                 120

cca ccc aga ctc ccc acc aag agg aag gcc tca gaa gag gct cga gct      556
Pro Pro Arg Leu Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala
125                 130                 135                 140

gcc gcg cca gca gcc ctg act cca agg ggc acc gcc agc cca ggc tct      604
Ala Ala Pro Ala Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser
                145                 150                 155

caa ctg aag gcc aag ccc ccc aag aag ccg gag agc agc gca gag cag      652
Gln Leu Lys Ala Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln
            160                 165                 170

cag cgc ctt cca ctc ggg aac ggg att cag acc atg tca gct tca gtc      700
Gln Arg Leu Pro Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val
        175                 180                 185

cag aga gct gtg gcc atg tcc tcc ggg gac gtc ccg gga gcc cga ggg      748
Gln Arg Ala Val Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly
    190                 195                 200

gcc gtg gag ggg atc ctc atc cag cag gtg ttt gag tca ggc ggc tcc      796
Ala Val Glu Gly Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser
205                 210                 215                 220

aag aag tgc atc cag gtt ggc ggg gag ttc tac act ccc agc aag ttc      844
Lys Lys Cys Ile Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe
                225                 230                 235

gaa gac tcc ggc agt ggg aag aac aag gcc cgc agc agc agt ggc ccg      892
Glu Asp Ser Gly Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro
            240                 245                 250
```

```
aag cct ctg gtt cga gcc aag gga gcc cag ggc gct gcc ccc ggt gga      940
Lys Pro Leu Val Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly
        255                 260                 265

ggt gag gct agg ctg ggc cag cag ggc agc gtt ccc gcc cct ctg gcc      988
Gly Glu Ala Arg Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala
    270                 275                 280

ctc ccc agt gac ccc cag ctc cac cag aag aat gag gac gag tgt gcc     1036
Leu Pro Ser Asp Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala
285                 290                 295                 300

gtg tgt cgg gac ggc ggg gag ctc atc tgc tgt gac ggc tgc cct cgg     1084
Val Cys Arg Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg
                305                 310                 315

gcc ttc cac ctg gcc tgc ctg tcc cct ccg ctc cgg gag atc ccc agt     1132
Ala Phe His Leu Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser
            320                 325                 330

ggg acc tgg agg tgc tcc agc tgc ctg cag gca aca gtc cag gag gtg     1180
Gly Thr Trp Arg Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val
        335                 340                 345

cag ccc cgg gca gag gag ccc cgg ccc cag gag cca ccc gtg gag acc     1228
Gln Pro Arg Ala Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr
    350                 355                 360

ccg ctc ccc ccg ggg ctt agg tcg gcg gga gag gag gta aga ggt cca     1276
Pro Leu Pro Pro Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro
365                 370                 375                 380

cct ggg gaa ccc cta gcc ggc atg gac acg act ctt gtc tac aag cac     1324
Pro Gly Glu Pro Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His
                385                 390                 395

ctg ccg gct ccg cct tct gca gcc ccg ctg cca ggg ctg gac tcc tcg     1372
Leu Pro Ala Pro Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser
            400                 405                 410

gcc ctg cac ccc cta ctg tgt gtg ggt cct gag ggt cag cag aac ctg     1420
Ala Leu His Pro Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu
        415                 420                 425

gct cct ggt gcg cgt tgc ggg gtg tgc gga gat ggt acg gac gtg ctg     1468
Ala Pro Gly Ala Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu
    430                 435                 440

cgg tgt act cac tgc gcc gct gcc ttc cac tgg cgc tgc cac ttc cca     1516
Arg Cys Thr His Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro
445                 450                 455                 460

gcc ggc acc tcc cgg ccc ggg acg ggc ctg cgc tgc aga tcc tgc tca     1564
Ala Gly Thr Ser Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser
```

```
                465                 470                 475

gga gac gtg acc cca gcc cct gtg gag ggg gtg ctg gcc ccc agc ccc     1612
Gly Asp Val Thr Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro
            480                 485                 490

gcc cgc ctg gcc cct ggg cct gcc aag gat gac act gcc agt cac gag     1660
Ala Arg Leu Ala Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu
        495                 500                 505

ccc gct ctg cac agg gat gac ctg gag tcc ctt ctg agc gag cac acc     1708
Pro Ala Leu His Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr
    510                 515                 520

ttc gat ggc atc ctg cag tgg gcc atc cag agc atg gcc cgt ccg gcg     1756
Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala
525                 530                 535                 540

gcc ccc ttc ccc tcc tgaccccaga tggccgggac atgcagctct gatgagagag     1811
Ala Pro Phe Pro Ser
                545

tgctgagaag gacacctcct tcctcagtcc tggaagccgg ccggctggga tcaagaaggg   1871

gacagcgcca cctcttgtca gtgctcggct gtaaacagct ctgtgtttct ggggacacca   1931

gccatcatgt gcctggaaat taaaccctgc cccacttctc tactctggaa gtccccggga   1991

gcctctcctt gcctggtgac ctactaaaaa tataaaaatt agctg                   2036
```

<210> 2
<211> 545
<212> PRT
<213> HOMO SAPIENS

<400> 2

```
Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr
1               5                   10                  15

Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
            20                  25                  30

Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
        35                  40                  45

Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
    50                  55                  60
```

```
Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
65                  70                  75                  80

Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
                85                  90                  95

Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
            100                 105                 110

Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
        115                 120                 125

Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
    130                 135                 140

Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
145                 150                 155                 160

Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
                165                 170                 175

Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
            180                 185                 190

Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
        195                 200                 205

Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
    210                 215                 220

Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
225                 230                 235                 240

Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
                245                 250                 255

Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
            260                 265                 270

Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
        275                 280                 285
```

Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp
290 295 300

Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
305 310 315 320

Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
325 330 335

Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
340 345 350

Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
355 360 365

Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
370 375 380

Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
385 390 395 400

Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
405 410 415

Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
420 425 430

Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
435 440 445

Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
450 455 460

Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
465 470 475 480

Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
485 490 495

Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His

```
            500                 505                 510

Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
        515                 520                 525

Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
    530                 535                 540

Ser
545
```

<210> 3
<211> 1545
<212> DNA
<213> HOMO SAPIENS

<220>
<221> CDS
<222> (237)..(1283)

<220>
<221> mat_peptide
<222> (1)..(348)
<223> /product="AIR-2"

<400> 3

```
agagaaagtg aggtcttctc aggctcttaa gagcatggcg tttggtccag gctgtacccg      60

ctgctctcag ctgggcccgt gggtgggccg ggcgcccctg ctatagccag gaggtcaagg     120

atccactggg aatgccatgc tcatctttcg tccccagcat ggtttcttaa tggggtagaa     180

gcaggtcggg agagacctcc ctgggcctgg ccccactgcc ctgtgaggaa gggttc atg     239
                                                                 Met
                                                                  1

tgg ttg gtg tac agt tcc ggg gcc cct gga acg cag cag cct gca aga       287
Trp Leu Val Tyr Ser Ser Gly Ala Pro Gly Thr Gln Gln Pro Ala Arg
            5                   10                  15

aac cgg gtt ttc ttc cca ata ggg atg gcc ccg ggg ggt gtc tgt tcg       335
Asn Arg Val Phe Phe Pro Ile Gly Met Ala Pro Gly Gly Val Cys Ser
        20                  25                  30

aga cca gat gga tgg gga aca ggt ggt cag ggc aga att tca ggc cct       383
Arg Pro Asp Gly Trp Gly Thr Gly Gly Gln Gly Arg Ile Ser Gly Pro
    35                  40                  45
```

```
ggc agc atg gga gca ggg cag aga ctg ggg agt tca ggt acc cag aga      431
Gly Ser Met Gly Ala Gly Gln Arg Leu Gly Ser Ser Gly Thr Gln Arg
50                  55                  60                  65

tgc tgc tgg ggg agc tgt ttt ggg aag gag gtg gct ctc agg agg gtg      479
Cys Cys Trp Gly Ser Cys Phe Gly Lys Glu Val Ala Leu Arg Arg Val
                70                  75                  80

ctg cac ccc agc cca gtc tgc atg ggc gtc tct tgc ctg tgc cag aag      527
Leu His Pro Ser Pro Val Cys Met Gly Val Ser Cys Leu Cys Gln Lys
            85                  90                  95

aat gag gac gag tgt gcc gtg tgt cgg gac ggc ggg gag ctc atc tgc      575
Asn Glu Asp Glu Cys Ala Val Cys Arg Asp Gly Gly Glu Leu Ile Cys
        100                 105                 110

tgt gac ggc tgc cct cgg gcc ttc cac ctg gcc tgc ctg tcc cct ccg      623
Cys Asp Gly Cys Pro Arg Ala Phe His Leu Ala Cys Leu Ser Pro Pro
    115                 120                 125

ctc cgg gag atc ccc agt ggg acc tgg agg tgc tcc agc tgc ctg cag      671
Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg Cys Ser Ser Cys Leu Gln
130                 135                 140                 145

gca aca gtc cag gag gtg cag ccc cgg gca gag gag ccc cgg ccc cag      719
Ala Thr Val Gln Glu Val Gln Pro Arg Ala Glu Glu Pro Arg Pro Gln
                150                 155                 160

gag cca ccc gtg gag acc ccg ctc ccc ccg ggg ctt agg tcg gcg gga      767
Glu Pro Pro Val Glu Thr Pro Leu Pro Pro Gly Leu Arg Ser Ala Gly
            165                 170                 175

gag gag gta aga ggt cca cct ggg gaa ccc cta gcc ggc atg gac acg      815
Glu Glu Val Arg Gly Pro Pro Gly Glu Pro Leu Ala Gly Met Asp Thr
        180                 185                 190

act ctt gtc tac aag cac ctg ccg gct ccg cct tct gca gcc ccg ctg      863
Thr Leu Val Tyr Lys His Leu Pro Ala Pro Pro Ser Ala Ala Pro Leu
    195                 200                 205

cca ggt ctg gac tcc tcg gcc ctg cac ccc cta ctg tgt gtg ggt cct      911
Pro Gly Leu Asp Ser Ser Ala Leu His Pro Leu Leu Cys Val Gly Pro
210                 215                 220                 225

gag ggt cag cag aac ctg gct cct ggt gcg cgt tgc ggg gtg tgc gga      959
Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala Arg Cys Gly Val Cys Gly
                230                 235                 240

gat ggt acg gac gtg ctg cgg tgt act cac tgc gcc gct gcc ttc cac     1007
Asp Gly Thr Asp Val Leu Arg Cys Thr His Cys Ala Ala Ala Phe His
            245                 250                 255

tgg cgc tgc cac ttc cca gcc ggc acc tcc cgg ccc ggg acg ggc ctg     1055
Trp Arg Cys His Phe Pro Ala Gly Thr Ser Arg Pro Gly Thr Gly Leu
```

```
        260                 265                 270

cgc tgc aga tcc tgc tca gga gac gtg acc cca gcc cct gtg gag ggg     1103
Arg Cys Arg Ser Cys Ser Gly Asp Val Thr Pro Ala Pro Val Glu Gly
    275                 280                 285

gtg ctg gcc ccc agc ccc gcc cgc ctg gcc cct ggg cct gcc aag gat     1151
Val Leu Ala Pro Ser Pro Ala Arg Leu Ala Pro Gly Pro Ala Lys Asp
290                 295                 300                 305

gac act gcc agt cac gag ccc gct ctg cac agg gat gac ctg gag tcc     1199
Asp Thr Ala Ser His Glu Pro Ala Leu His Arg Asp Asp Leu Glu Ser
                310                 315                 320

ctt ctg agc gag cac acc ttc gat ggc atc ctg cag tgg gcc atc cag     1247
Leu Leu Ser Glu His Thr Phe Asp Gly Ile Leu Gln Trp Ala Ile Gln
            325                 330                 335

agc atg gcc cgt ccg gcg gcc ccc ttc ccc tcc tga ccccagatgg          1293
Ser Met Ala Arg Pro Ala Ala Pro Phe Pro Ser
        340                 345

ccgggacatg cagctctgat gagagagtgc tgagaaggac acctccttcc tcagtcctgg   1353

aagccggccg gctgggatca agaaggggac agcgccacct cttgtcagtg ctcggctgta   1413

aacagctctg tgtttctggg gacaccagcc atcatgtgcc tggaaattaa accctgcccc   1473

acttctctac tctggaagtc cccgggagcc tctccttgcc tggtgaccta ctaaaaatat   1533

aaaaattagc tg                                                       1545
```

<210> 4
<211> 348
<212> PRT
<213> HOMO SAPIENS

<400> 4

```
Met Trp Leu Val Tyr Ser Ser Gly Ala Pro Gly Thr Gln Gln Pro Ala
1               5                   10                  15

Arg Asn Arg Val Phe Phe Pro Ile Gly Met Ala Pro Gly Gly Val Cys
            20                  25                  30

Ser Arg Pro Asp Gly Trp Gly Thr Gly Gly Gln Gly Arg Ile Ser Gly
        35                  40                  45

Pro Gly Ser Met Gly Ala Gly Gln Arg Leu Gly Ser Ser Gly Thr Gln
    50                  55                  60
```

```
Arg Cys Cys Trp Gly Ser Cys Phe Gly Lys Glu Val Ala Leu Arg Arg
65                  70                  75                  80

Val Leu His Pro Ser Pro Val Cys Met Gly Val Ser Cys Leu Cys Gln
                85                  90                  95

Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp Gly Gly Glu Leu Ile
            100                 105                 110

Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu Ala Cys Leu Ser Pro
        115                 120                 125

Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg Cys Ser Ser Cys Leu
    130                 135                 140

Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala Glu Glu Pro Arg Pro
145                 150                 155                 160

Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro Gly Leu Arg Ser Ala
                165                 170                 175

Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro Leu Ala Gly Met Asp
            180                 185                 190

Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro Pro Ser Ala Ala Pro
        195                 200                 205

Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro Leu Leu Cys Val Gly
    210                 215                 220

Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala Arg Cys Gly Val Cys
225                 230                 235                 240

Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His Cys Ala Ala Ala Phe
                245                 250                 255

His Trp Arg Cys His Phe Pro Ala Gly Thr Ser Arg Pro Gly Thr Gly
            260                 265                 270

Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr Pro Ala Pro Val Glu
```

```
        275                 280                 285

Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala Pro Gly Pro Ala Lys
    290                 295                 300

Asp Asp Thr Ala Ser His Glu Pro Ala Leu His Arg Asp Asp Leu Glu
305                 310                 315                 320

Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile Leu Gln Trp Ala Ile
                325                 330                 335

Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro Ser
            340                 345
```

<210> 5
<211> 1463
<212> DNA
<213> HOMO SAPIENS

<220>
<221> CDS
<222> (237)..(1001)
<223> /product=:AIR-3"

<220>
<221> mat_peptide
<222> (1)..(254)
<223> /product="AIR-3"

<400> 5

```
agagaaagtg aggtcttctc aggctcttaa gagcatggcg tttggtccag gctgtacccg     60

ctgctctcag ctgggcccgt gggtgggccg ggcgcccctg ctatagccag gaggtcaagg    120

atccactggg aatgccatgc tcatctttcg tccccagcat ggtttcttaa tggggtagaa    180

gcaggtcggg agagacctcc ctgggcctgg ccccactgcc ctgtgaggaa gggttc atg    239
                                                                 Met
                                                                  1

tgg ttg gtg tac agt tcc ggg gcc cct gga acg cag cag cct gca aga      287
Trp Leu Val Tyr Ser Ser Gly Ala Pro Gly Thr Gln Gln Pro Ala Arg
            5                   10                  15

aac cgg gtt ttc ttc cca ata ggg atg gcc ccg ggg ggt gtc tgt tgg      335
Asn Arg Val Phe Phe Pro Ile Gly Met Ala Pro Gly Gly Val Cys Trp
```

```
        20                  25                  30

aga cca gat gga tgg gga aca ggt ggt cag ggc aga att tca ggc cct      383
Arg Pro Asp Gly Trp Gly Thr Gly Gly Gln Gly Arg Ile Ser Gly Pro
    35                  40                  45

ggc agc atg gga gca ggg cag aga ctg ggg agt tca ggt acc cag aga      431
Gly Ser Met Gly Ala Gly Gln Arg Leu Gly Ser Ser Gly Thr Gln Arg
50                  55                  60                  65

tgc tgc tgg ggg agc tgt ttt ggg aag gag gtg gct ctc agg agg gtg      479
Cys Cys Trp Gly Ser Cys Phe Gly Lys Glu Val Ala Leu Arg Arg Val
                70                  75                  80

ctg cac ccc agc cca gtc tgc atg ggc gtc tct tgc ctg tgc cag aag      527
Leu His Pro Ser Pro Val Cys Met Gly Val Ser Cys Leu Cys Gln Lys
            85                  90                  95

aat gag gac gag tgt gcc gtg tgt cgg gac ggc ggg gag ctc atc tgc      575
Asn Glu Asp Glu Cys Ala Val Cys Arg Asp Gly Gly Glu Leu Ile Cys
        100                 105                 110

tgt gac ggc tgc cct cgg gcc ttc cac ctg gcc tgc ctg tcc cct ccg      623
Cys Asp Gly Cys Pro Arg Ala Phe His Leu Ala Cys Leu Ser Pro Pro
    115                 120                 125

ctc cgg gag atc ccc agt ggg acc tgg agg tgc tcc agc tgc ctg cag      671
Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg Cys Ser Ser Cys Leu Gln
130                 135                 140                 145

gca aca gtc cag gag gtg cag ccc cgg gca gag gag ccc cgg ccc cag      719
Ala Thr Val Gln Glu Val Gln Pro Arg Ala Glu Glu Pro Arg Pro Gln
                150                 155                 160

gag cca ccc gtg gag acc ccg ctc ccc ccg ggg ctt agg tcg gcg gga      767
Glu Pro Pro Val Glu Thr Pro Leu Pro Pro Gly Leu Arg Ser Ala Gly
            165                 170                 175

gag gag ccc cgc tgc cag ggc tgg act cct cgg ccc tgc acc ccc tac      815
Glu Glu Pro Arg Cys Gln Gly Trp Thr Pro Arg Pro Cys Thr Pro Tyr
        180                 185                 190

tgt gtg tgg gtc ctg agg gtc agc aga acc tgg ctc ctg gtg cgc gtt      863
Cys Val Trp Val Leu Arg Val Ser Arg Thr Trp Leu Leu Val Arg Val
    195                 200                 205

gcg ggg tgt gcg gag atg gta cgg acg tgc tgc ggt gta ctc act gcg      911
Ala Gly Cys Ala Glu Met Val Arg Thr Cys Cys Gly Val Leu Thr Ala
210                 215                 220                 225

ccg ctg cct tcc act ggc gct gcc act tcc cag ccg gca cct ccc ggc      959
Pro Leu Pro Ser Thr Gly Ala Ala Thr Ser Gln Pro Ala Pro Pro Gly
                230                 235                 240
```

```
ccg gga cgg gcc tgc gct gca gat cct gct cag gag acg tga                1001
Pro Gly Arg Ala Cys Ala Ala Asp Pro Ala Gln Glu Thr
            245                 250

ccccagcccc tgtggagggg gtgctggccc ccagccccgc ccgcctggcc cctgggcctg     1061

ccaaggatga cactgccagt cacgagcccg ctctgcacag ggatgacctg gagtcccttc     1121

tgagcgagca caccttcgat ggcatcctgc agtgggccat ccagagcatg gcccgtccgg     1181

cggccccctt cccctcctga ccccagatgg ccgggacatg cagctctgat gagagagtgc     1241

tgagaaggac acctccttcc tcagtcctgg aagccggccg gctgggatca agaaggggac     1301

agcgccacct cttgtcagtg ctcggctgta aacagctctg tgtttctggg gacaccagcc     1361

atcatgtgcc tggaaattaa accctgcccc acttctctac tctggaagtc cccgggagcc     1421

tctccttgcc tggtgaccta ctaaaaatat aaaaattagc tg                        1463
```

<210> 6
<211> 254
<212> PRT
<213> HOMO SAPIENS

<400> 6

```
Met Trp Leu Val Tyr Ser Ser Gly Ala Pro Gly Thr Gln Gln Pro Ala
1               5                  10                  15

Arg Asn Arg Val Phe Phe Pro Ile Gly Met Ala Pro Gly Gly Val Cys
            20                  25                  30

Trp Arg Pro Asp Gly Trp Gly Thr Gly Gly Gln Gly Arg Ile Ser Gly
        35                  40                  45

Pro Gly Ser Met Gly Ala Gly Gln Arg Leu Gly Ser Ser Gly Thr Gln
    50                  55                  60

Arg Cys Cys Trp Gly Ser Cys Phe Gly Lys Glu Val Ala Leu Arg Arg
65                  70                  75                  80

Val Leu His Pro Ser Pro Val Cys Met Gly Val Ser Cys Leu Cys Gln
                85                  90                  95

Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp Gly Gly Glu Leu Ile
            100                 105                 110
```

Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu Ala Cys Leu Ser Pro
115 120 125

Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg Cys Ser Ser Cys Leu
130 135 140

Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala Glu Glu Pro Arg Pro
145 150 155 160

Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro Gly Leu Arg Ser Ala
165 170 175

Gly Glu Glu Pro Arg Cys Gln Gly Trp Thr Pro Arg Pro Cys Thr Pro
180 185 190

Tyr Cys Val Trp Val Leu Arg Val Ser Arg Thr Trp Leu Leu Val Arg
195 200 205

Val Ala Gly Cys Ala Glu Met Val Arg Thr Cys Cys Gly Val Leu Thr
210 215 220

Ala Pro Leu Pro Ser Thr Gly Ala Ala Thr Ser Gln Pro Ala Pro Pro
225 230 235 240

Gly Pro Gly Arg Ala Cys Ala Ala Asp Pro Ala Gln Glu Thr
245 250

<210> 7
<211> 20
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 7
gatgacactg ccagtcacga 20

<210> 8
<211> 22
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 8
gttcccgagt ggaaggcgct gc 22

<210> 9
<211> 20
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 9
aggggacagg caggccaggt 20

<210> 10
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 10
gagttcaggt acccagagat gctg 24

<210> 11
<211> 20
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 11
ctcgctcaga agggactcca 20

<210> 12
<211> 23
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 12
ggattcagac catgtcagct tca 23

<210> 13
<211> 21
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 13
gtgctgttca aggatcacaa c 21

<210> 14
<211> 21
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 14
tggatgagga tcccctccac g 21

<210> 15
<211> 27
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 15
ccatcctaat acgactcact atagggc 27

<210> 16
<211> 20
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 16
tgcaggctgt gggaactcca 20

<210> 17
<211> 22
<212> DNA
<213> ARTIFICIAL

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 17
agaaaaagag ctgtaccctg tg 22

<210> 18
<211> 22
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 18
tgcaaggaag aggggcgtca gc 22

<210> 19
<211> 21
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 19
tccaccacaa gccgaggaga t 21

<210> 20
<211> 21
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 20
acgggctcct caaacaccac t 21

<210> 21
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 21
tggagatggg caggccgcag ggtg 24

<210> 22
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 22
cagtccagct gggctgagca ggtg 24

<210> 23
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 23
gcggctccaa gaagtgcatc cagg 24

<210> 24
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 24
ctccaccctg caaggaagag gggc 24

<210> 25
<211> 16
<212> PRT
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 25

Thr Leu His Leu Lys Glu Lys Glu Gly Cys Pro Val Gln Ala Phe His
1 5 10 15

<210> 26
<211> 15
<212> PRT
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 26

Cys Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
1 5 10 15

<210> 27
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 27
atggcgacgg acgcggcgct acgc 24

<210> 28
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 28
cctggatgta cttcttggag ccgc 24

<210> 29
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 29
gagcccgagg ggccgtggag ggga 24

<210> 30
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 30

ggctgcacct cctggactgt tgcc 24

<210> 31
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 31
gatcctgctc aggagacgtg accc 24

<210> 32
<211> 24
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 32
caccaggcaa ggagaggctc ccgg 24

<210> 33
<211> 20
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 33
ccaccccatg gcgacggacg 20

<210> 34
<211> 29
<212> DNA
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 34
ggaattcgga ggggaagggg gccgccgga 29

<210> 35
<211> 24
<212> DNA

<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 35
ggactgagga aggaggtgtc cttc 24

<210> 36
<211> 20
<212> PRT
<213> ARTIFICIAL

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 36

Asp Gly Ile Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala
1 5 10 15

Pro Phe Pro Ser
20

<210> 37
<211> 42
<212> PRT
<213> Homo sapiens

<400> 37

Cys Ala Val Cys Arg Asp Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys
1 5 10 15

Pro Arg Ala Phe His Leu Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile
20 25 30

Pro Ser Gly Thr Trp Arg Cys Ser Ser Cys
35 40

<210> 38
<211> 42
<212> PRT
<213> HOMO SAPIENS

<400> 38

```
Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His Cys
1               5                   10                  15

Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser Arg
            20                  25                  30

Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys
        35                  40
```

<210> 39
<211> 42
<212> PRT
<213> HOMO SAPIENS

<400> 39

```
Cys Glu Val Cys Gln Gln Gly Gly Glu Ile Ile Leu Cys Asp Thr Cys
1               5                   10                  15

Pro Arg Ala Thr His Met Val Cys Leu Asp Pro Asp Met Glu Lys Ala
            20                  25                  30

Pro Glu Gly Leu Trp Ser Cys Pro His Cys
        35                  40
```

<210> 40
<211> 42
<212> PRT
<213> HOMO SAPIENS

<400> 40

```
Cys Arg Val Cys Lys Asp Gly Gly Glu Leu Ile Cys Cys Asp Thr Cys
1               5                   10                  15

Pro Ser Ser Tyr His Ile His Cys Leu Asn Pro Pro Leu Pro Glu Ile
            20                  25                  30

Pro Asn Gly Glu Trp Leu Cys Pro Arg Cys
        35                  40
```

<210> 41
<211> 42
<212> PRT
<213> HOMO SAPIENS

<400> 41

Cys Ala Val Cys Gln Asn Gly Gly Glu Leu Ile Cys Cys Glu Lys Cys
1 5 10 15

Pro Lys Val Phe His Leu Ser Cys His Val Pro Thr Leu Thr Asn Phe
20 25 30

Pro Ser Gly Glu Trp Ile Cys Thr Phe Cys
35 40